



SEQUENCE LISTING

<110> Kelly, Kathleen
The Government of the United States of America
as represented by The Secretary of the
Department of Health and Human Services

<120> Methods and Compositions for Inhibiting Inflammation
and Angiogenesis Comprising a Mammalian CD97 Alpha
Subunit

<130> 015280-263100US

<140> US 09/284,819

<141> 1999-08-20

<150> US 60/027,871

<151> 1996-10-25

<150> WO PCT/US97/19772

<151> 1997-10-24

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-1 EGF-like
repeat conserved motif

<400> 1

Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln Asn Ser Ser Cys Val
1 5 10 15

Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe Ser Ser Phe Ser Glu
20 25 30

Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp
35 40

<210> 2

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-2 EGF-like
repeat conserved motif

<400> 2

Asp Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe
1 5 10 15

Ser Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro
20 25 30

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Gly Tyr Glu Pro Val Ser Gly Thr Lys Thr Phe Lys Asn Glu Ser Glu
35 40 45

Asn Thr Cys Gln
50

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<210> 3
<211> 44
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:EGF-3 EGF-like
repeat conserved motif
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<400> 3
Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys Ser Tyr Gly
  1                    5                10                15
Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys Leu Pro Gly
          20                25                30
Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr
      35                40

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<210> 4
<211> 49
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:EGF-4 EGF-like
repeat conserved motif
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<400> 4
Asp Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr
  1             5             10             15
His Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly
          20             25             30
Trp Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys
      35             40             45

```

Glu

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<210> 5
<211> 49
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence:EGF-5 EGF-like
repeat conserved motif
```

<400> 5
Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr
1 5 10 15

Val Cys Phe Asn Thr Val Gly Ser Tyr Ser Cys Arg Cys Arg Pro Gly
 20 25 30

Trp Lys Pro Arg His Gly Ile Pro Asn Asn Gln Lys Asp Thr Val Cys
 35 40 45

Glu

<210> 6
 <211> 835
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CD97amino acid sequence encoded by full-length
 clone pAT276

<400> 6
 Met Gly Gly Arg Val Phe Leu Ala Phe Cys Val Trp Leu Thr Leu Pro
 1 5 10 15

Gly Ala Glu Thr Gln Asp Ser Arg Gly Cys Ala Arg Trp Cys Pro Gln
 20 25 30

Asn Ser Ser Cys Val Asn Ala Thr Ala Cys Arg Cys Asn Pro Gly Phe
 35 40 45

Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Thr Glu Thr Cys Asp Asp
 50 55 60

Ile Asn Glu Cys Ala Thr Pro Ser Lys Val Ser Cys Gly Lys Phe Ser
 65 70 75 80

Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys Ser Pro Gly
 85 90 95

Tyr Glu Pro Val Ser Gly Thr Lys Thr Phe Lys Asn Glu Ser Glu Asn
 100 105 110

Thr Cys Gln Asp Val Asp Glu Cys Gln Gln Asn Pro Arg Leu Cys Lys
 115 120 125

Ser Tyr Gly Thr Cys Val Asn Thr Leu Gly Ser Tyr Thr Cys Gln Cys
 130 135 140

Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys Thr Asp
 145 150 155 160

Val Asn Glu Cys Thr Ser Gly Gln Asn Pro Cys His Ser Ser Thr His
 165 170 175

Cys Leu Asn Asn Val Gly Ser Tyr Gln Cys Arg Cys Arg Pro Gly Trp
 180 185 190

Gln Pro Ile Pro Gly Ser Pro Asn Gly Pro Asn Asn Thr Val Cys Glu
 195 200 205

Asp Val Asp Glu Cys Ser Ser Gly Gln His Gln Cys Asp Ser Ser Thr
 210 215 220

Val	Cys	Phe	Asn	Thr	Val	Gly	Ser	Tyr	Ser	Cys	Arg	Cys	Arg	Pro	Gly	225	230	235	240
Trp	Lys	Pro	Arg	His	Gly	Ile	Pro	Asn	Asn	Gln	Lys	Asp	Thr	Val	Cys	245	250		255
Glu	Asp	Met	Thr	Phe	Ser	Thr	Trp	Thr	Pro	Pro	Pro	Gly	Val	His	Ser	260	265		270
Gln	Thr	Leu	Ser	Arg	Phe	Phe	Asp	Lys	Val	Gln	Asp	Leu	Gly	Arg	Asp	275	280	285	
Ser	Lys	Thr	Ser	Ser	Ala	Glu	Val	Thr	Ile	Gln	Asn	Val	Ile	Lys	Leu	290	295	300	
Val	Asp	Glu	Leu	Met	Glu	Ala	Pro	Gly	Asp	Val	Glu	Ala	Leu	Ala	Pro	305	310	315	320
Pro	Val	Arg	His	Leu	Ile	Ala	Thr	Gln	Leu	Leu	Ser	Asn	Leu	Glu	Asp	325	330		335
Ile	Met	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Pro	Lys	Gly	Pro	Phe	Thr	Tyr	340	345		350
Ile	Ser	Pro	Ser	Asn	Thr	Glu	Leu	Thr	Leu	Met	Ile	Gln	Glu	Arg	Gly	355	360	365	
Asp	Lys	Asn	Val	Thr	Met	Gly	Gln	Ser	Ser	Ala	Arg	Met	Lys	Leu	Asn	370	375	380	
Trp	Ala	Val	Ala	Ala	Gly	Ala	Glu	Asp	Pro	Gly	Pro	Ala	Val	Ala	Gly	385	390	395	400
Ile	Leu	Ser	Ile	Gln	Asn	Met	Thr	Thr	Leu	Leu	Ala	Asn	Ala	Ser	Leu	405	410		415
Asn	Leu	His	Ser	Lys	Lys	Gln	Ala	Glu	Leu	Glu	Glu	Ile	Tyr	Glu	Ser	420	425	430	
Ser	Ile	Arg	Gly	Val	Gln	Leu	Arg	Arg	Leu	Ser	Ala	Val	Asn	Ser	Ile	435	440	445	
Phe	Leu	Ser	His	Asn	Asn	Thr	Lys	Glu	Leu	Asn	Ser	Pro	Ile	Leu	Phe	450	455	460	
Ala	Phe	Ser	His	Leu	Glu	Ser	Ser	Asp	Gly	Glu	Ala	Gly	Arg	Asp	Pro	465	470	475	480
Pro	Ala	Lys	Asp	Val	Met	Pro	Gly	Pro	Arg	Gln	Glu	Leu	Leu	Cys	Ala	485	490	495	
Phe	Trp	Lys	Ser	Asp	Ser	Asp	Arg	Gly	Gly	His	Trp	Ala	Thr	Glu	Gly	500	505	510	
Cys	Gln	Val	Leu	Gly	Ser	Lys	Asn	Gly	Ser	Thr	Thr	Cys	Gln	Cys	Ser	515	520	525	
His	Leu	Ser	Ser	Phe	Ala	Ile	Leu	Met	Ala	His	Tyr	Asp	Val	Glu	Asp	530	535	540	

Trp Lys Leu Thr Leu Ile Thr Arg Val Gly Leu Ala Leu Ser Leu Phe
 545 550 555 560
 Cys Leu Leu Leu Cys Ile Leu Thr Phe Leu Leu Val Arg Pro Ile Gln
 565 570 575
 Gly Ser Arg Thr Thr Ile His Leu His Leu Cys Ile Cys Leu Phe Val
 580 585 590
 Gly Ser Thr Ile Phe Leu Ala Gly Ile Glu Asn Glu Gly Gly Gln Val
 595 600 605
 Gly Leu Arg Cys Arg Leu Val Ala Gly Leu Leu His Tyr Cys Phe Leu
 610 615 620
 Ala Ala Phe Cys Trp Met Ser Leu Glu Gly Leu Glu Leu Tyr Phe Leu
 625 630 635 640
 Val Val Arg Val Phe Gln Gly Gln Gly Leu Ser Thr Arg Trp Leu Cys
 645 650 655
 Leu Ile Gly Tyr Gly Val Pro Leu Leu Ile Val Gly Val Ser Ala Ala
 660 665 670
 Ile Tyr Ser Lys Gly Tyr Gly Arg Pro Arg Tyr Cys Trp Leu Asp Phe
 675 680 685
 Glu Gln Gly Phe Leu Trp Ser Phe Leu Gly Pro Val Thr Phe Ile Ile
 690 695 700
 Leu Cys Asn Ala Val Ile Phe Val Thr Thr Val Trp Lys Leu Thr Gln
 705 710 715 720
 Lys Phe Ser Glu Ile Asn Pro Asp Met Lys Lys Leu Lys Lys Ala Arg
 725 730 735
 Ala Leu Thr Ile Thr Ala Ile Ala Gln Leu Phe Leu Leu Gly Cys Thr
 740 745 750
 Trp Val Phe Gly Leu Phe Ile Phe Asp Asp Arg Ser Leu Val Leu Thr
 755 760 765
 Tyr Val Phe Thr Ile Leu Asn Cys Leu Gln Gly Ala Phe Leu Tyr Leu
 770 775 780
 Leu His Cys Leu Leu Asn Lys Lys Val Arg Glu Glu Tyr Arg Lys Trp
 785 790 795 800
 Ala Cys Leu Val Ala Gly Gly Ser Lys Tyr Ser Glu Phe Thr Ser Thr
 805 810 815
 Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala Leu Arg Ala Ser Glu
 820 825 830
 Ser Gly Ile
 835

<210> 7
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RGD motif
 binding site for several classes of integrins

<400> 7
 Arg Gly Asp
 1

<210> 8
 <211> 3156
 <212> DNA
 <213> Homo sapiens

<220>
 <223> full length pAT276 encoding CD97

<220>
 <221> CDS
 <222> (49)..(2556)
 <223> CD97

<400> 8
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 ggtgtgtccc ggtggtgccc tcagaactcc tcgtgtgtca atgccaccgc ctgtcgctgc 180
 aatccagggt tcagctcttt ttctgagatc atcaccaccc cgacgggagac ttgtgacgac 240
 atcaacgagt gtgcaacacc gtcgaaagtg tcatgcggaa aattctcgga ctgctggaac 300
 acagagggga gctacgactg cgtgtgcagc ccgggatatg agcctgtttc tgggacaaaa 360
 acattcaaga atgagagcga gaacacctgt caagatgtgg acgaatgtca gcagaaccca 420
 aggctctgta aaagctacgg cacctgcgtc aacacccttg gcagctatac ctgccagtgc 480
 ctgcctggct tcaagttcat acctgaggat ccgaaggctc gcacagatgt gaatgaatgc 540
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 cacggaatcc cgaataacca aaaggacact gtctgtgaag atatgacttt ctccacctgg 840
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tggttggaact ttgagcaggg cttcctctgg agcttcttgg gacctgtgac cttcatcatt 2160
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<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Description of Artificial Sequence:5' PCR primer
276-38

```

```

<400> 9
ggccgcgtct ttctcgca 18

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```

<210> 10
<211> 17
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:5' PCR primer
276-20

```

```

<400> 10
agatgtggac gaatgtc 17

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```

<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:5' PCR primer
276-6A

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<400> 11
aagacaagct cagccga 17

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<210> 12
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' PCR primer
 276-3

<400> 12
 tgggttcata cagctgc

17

<210> 13
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' PCR primer
 276-6B

<400> 13
 tcggctgagc ttgtctt

17

<210> 14
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' PCR primer
 276-15B

<400> 14
 gcagctgtat gaaccca

17

<210> 15
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:anti-EGF3
 peptide used for antibody production

<400> 15
 Cys Leu Pro Gly Phe Lys Phe Ile Pro Glu Asp Pro Lys Val Cys
 1 5 10 15

<210> 16
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:anti-COOH
 peptide used for antibody production

<400> 16

Glu Phe Thr Ser Thr Thr Ser Gly Thr Gly His Asn Gln Thr Arg Ala
 1 5 10 15

<210> 17

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide
 amplification primer

<400> 17

atgggaggcc gcgtctttct cgcattctgt gt

32

<210> 18

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide
 amplification primer

<400> 18

gggccctcag ggcacagag tccggcata

29

<210> 19

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-like repeat
 conserved motif in fibrillin

<220>

<221> MOD_RES

<222> (1)..(41)

<223> Xaa = any amino acid

<400> 19

Asp Ile Asp Glu Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Gly Xaa
 1 5 10 15

Cys Xaa Asn Thr Xaa Gly Ser Tyr Xaa Cys Xaa Cys Xaa Xaa Gly Phe
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 35 40

<210> 20

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EGF-like repeat
conserved motif in EMR1

<220>

<221> MOD_RES

<222> (1)..(48)

<223> Xaa = any amino acid

<400> 20

Asp Ile Asp Glu Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Cys Xaa Asn Xaa Xaa Gly Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa Gly
20 25 30

Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
35 40 45

<210> 21

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Asp/Asn
beta-hydroxylation consensus motif

<220>

<221> MOD_RES

<222> (1)..(12)

<223> Xaa = any amino acid

<400> 21

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys
1 5 10